

RAW SEQUENCE LISTING

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Application Serial Number: 10/ 523,912

Source: PCT

Date Processed by STIC: 2-22-05

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PCT

RAW SEQUENCE LISTING

DATE: 02/22/2005

PATENT APPLICATION: US/10/523,912

TIME: 09:19:58

Input Set : A:\PTO.SR.txt

Output Set: N:\CRF4\02222005\J523912.raw

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 9 <110> APPLICANT: Dron, Michel
13      Meritet, Jean-FranTois
17      Tovey, Michael Gerard
29 <120> TITLE OF INVENTION: INTERFERON-ALPHA INDUCED GENE
37 <130> FILE REFERENCE: 046658/288239
C--> 45 <140> CURRENT APPLICATION NUMBER: US/10/523,912
C--> 45 <141> CURRENT FILING DATE: 2005-02-08
45 <150> PRIOR APPLICATION NUMBER: GB 0218473.7
49 <151> PRIOR FILING DATE: 2002-08-08
57 <160> NUMBER OF SEQ ID NOS: 4
65 <170> SOFTWARE: PatentIn version 3.0
73 <210> SEQ ID NO: 1
77 <211> LENGTH: 8157
81 <212> TYPE: DNA
85 <213> ORGANISM: HOMO SAPIENS
93 <220> FEATURE:
97 <221> NAME/KEY: CDS
101 <222> LOCATION: (101)..(5902)
105 <223> OTHER INFORMATION:
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125 tggcgcgcc cctgcagtcc ggcgagagc ggagctgagg atg gct gtg ccc ggc      115
129                                     Met Ala Val Pro Gly
133                                     1          5
141 tcc ttc ccg ctg ctg gtc gag ggc tcc tgg ggc ccc gac ccc ccg aag      163
145 Ser Phe Pro Leu Leu Val Glu Gly Ser Trp Gly Pro Asp Pro Pro Lys
149          10          15          20
157 aac ttg aac acc aag ttg cag atg tac ttc cag agc ccg aag agg tcg      211
161 Asn Leu Asn Thr Lys Leu Gln Met Tyr Phe Gln Ser Pro Lys Arg Ser
165          25          30          35
173 gga ggc ggc gag tgt gag gtc cgc cag gat ccc agg agc cca tcc cgc      259
177 Gly Gly Gly Glu Cys Glu Val Arg Gln Asp Pro Arg Ser Pro Ser Arg
181          40          45          50
189 ttc ctg gtg ttc ttc tac ccg gag gac ggg aaa tgg cgg cag ggc acg      307
193 Phe Leu Val Phe Phe Tyr Pro Glu Asp Gly Lys Trp Arg Gln Gly Thr
197          55          60          65
205 cac ggg agg gtg acc cgc ccg act tcg gcg gct gct gta gcg gag gcg      355
209 His Gly Arg Val Thr Arg Pro Thr Ser Ala Ala Ala Val Ala Glu Ala
213 70          75          80          85
221 ctt aat ggc gcg gcc cgg agg tgg cgg cgg aac cgc gca agt aac tct      403
225 Leu Asn Gly Ala Ala Arg Arg Trp Arg Arg Asn Arg Ala Ser Asn Ser
229          90          95          100
237 tta tcc ctc gat cgt ttt ctg tct ttc cct gtt gtg gtg tta ttg      451

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261			120					125					130				
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289	Lys	Lys	Arg	Gly	Lys	Ser	Gln	Arg	Phe	Leu	Val	Val	Leu	Gly	Asp	Ser	
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301	cag	ggg	tcc	cgg	ggt	cac	ttg	gga	gag	ggg	cag	agg	cgc	tac	cta	aaa	643
305	Gln	Gly	Ser	Arg	Gly	His	Leu	Gly	Glu	Gly	Gln	Arg	Arg	Tyr	Leu	Lys	
309					170					175					180		
317	tca	cac	tgc	ctg	aat	gtc	aac	gta	gag	ccg	tca	cag	cgg	cca	cat	tgg	691
321	Ser	His	Cys	Leu	Asn	Val	Asn	Val	Glu	Pro	Ser	Gln	Arg	Pro	His	Trp	
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333	agg	ggc	tgt	cga	tcg	acc	aca	gtt	cgg	cag	aag	gtt	ctg	gag	aga	aaa	739
337	Arg	Gly	Cys	Arg	Ser	Thr	Thr	Val	Arg	Gln	Lys	Val	Leu	Glu	Arg	Lys	
341			200					205					210				
349	aat	cat	gag	ttg	gta	tgg	caa	gga	aaa	gga	aca	ttc	aag	tta	act	gtc	787
353	Asn	His	Glu	Leu	Val	Trp	Gln	Gly	Lys	Gly	Thr	Phe	Lys	Leu	Thr	Val	
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365	cag	tta	cct	gca	acc	cca	gat	gaa	atc	gat	cat	gtc	ttt	gaa	gag	gaa	835
369	Gln	Leu	Pro	Ala	Thr	Pro	Asp	Glu	Ile	Asp	His	Val	Phe	Glu	Glu	Glu	
373	230					235					240				245		
381	ctt	cta	aca	aaa	gca	aat	gtg	tca	gaa	gaa	ttg	gat	aca	aaa	ctc	cct	883
385	Leu	Leu	Thr	Lys	Ala	Asn	Val	Ser	Glu	Glu	Leu	Asp	Thr	Lys	Leu	Pro	
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397	ctt	gat	ggt	gga	tta	gac	aaa	atg	gaa	gat	atc	cca	gag	gaa	tgt	gaa	931
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413	aat	att	tcc	tct	ttg	gtg	gca	ttt	gaa	aac	ctc	aag	gca	aat	gtg	act	979
417	Asn	Ile	Ser	Ser	Leu	Val	Ala	Phe	Glu	Asn	Leu	Lys	Ala	Asn	Val	Thr	
421			280					285					290				
429	gac	ata	atg	cta	atc	ttg	tta	gtg	gag	aac	ata	agt	ggc	ctg	tct	aat	1027
433	Asp	Ile	Met	Leu	Ile	Leu	Val	Glu	Asn	Ile	Ser	Gly	Leu	Ser	Asn		
437		295				300					305						
445	gat	gac	ttt	caa	gtg	gaa	ata	ata	aga	gat	ttt	gat	gtt	gct	gtt	gtt	1075
449	Asp	Asp	Phe	Gln	Val	Glu	Ile	Ile	Arg	Asp	Phe	Asp	Val	Ala	Val	Val	
453	310				315					320				325			
461	acc	ttt	caa	aag	cac	ata	gat	act	ata	aga	ttt	gtt	gat	gat	tgt	acc	1123
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469				330					335				340				
477	aag	cac	cat	tca	att	aaa	caa	ctt	cag	ctt	tct	cca	aga	ctt	ctg	gaa	1171
481	Lys	His	His	Ser	Ile	Lys	Gln	Leu	Gln	Leu	Ser	Pro	Arg	Leu	Leu	Glu	
485			345					350					355				
493	gtg	aca	aac	aca	atc	agg	gtt	gaa	aac	ctg	cca	cct	ggt	gct	gat	gac	1219
497	Val	Thr	Asn	Thr	Ile	Arg	Val	Glu	Asn	Leu	Pro	Pro	Gly	Ala	Asp	Asp	

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525	ggt gcc aat gtt gaa tat ttt cct gaa gag agt tca gct ctg att gaa	1315		
529	Val Ala Asn Val Glu Tyr Phe Pro Glu Glu Ser Ser Ala Leu Ile Glu			
533	390 395 400 405			
541	ttt ttt gac aga aaa gtg tta gac acc atc atg gcc aca aaa ctc gac	1363		
545	Phe Phe Asp Arg Lys Val Leu Asp Thr Ile Met Ala Thr Lys Leu Asp			
549	410 415 420			
557	ttc aat aaa atg cca ctt tct gtg ttc cca tac tat gcc tca ttg ggc	1411		
561	Phe Asn Lys Met Pro Leu Ser Val Phe Pro Tyr Tyr Ala Ser Leu Gly			
565	425 430 435			
573	aca gcc ttg tat gga aag gag aag cct ctg atc aag ctt cca gca cca	1459		
577	Thr Ala Leu Tyr Gly Lys Glu Lys Pro Leu Ile Lys Leu Pro Ala Pro			
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589	ttt gaa gag tca cta gat ctt ccc tta tgg aag ttc tta cag aaa aag	1507		
593	Phe Glu Glu Ser Leu Asp Leu Pro Leu Trp Lys Phe Leu Gln Lys Lys			
597	455 460 465			
605	aat cac ctc att gag gag ata aac gat gaa atg agg cgt tgt cac tgt	1555		
609	Asn His Leu Ile Glu Glu Ile Asn Asp Glu Met Arg Arg Cys His Cys			
613	470 475 480 485			
621	gag ctc acg tgg tcc caa ctc agt ggt aaa gtt acc atc aga cca gca	1603		
625	Glu Leu Thr Trp Ser Gln Leu Ser Gly Lys Val Thr Ile Arg Pro Ala			
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637	gcc acc tta gtc aat gaa gga aga ccg aga atc aag acc tgg cag gca	1651		
641	Ala Thr Leu Val Asn Glu Gly Arg Pro Arg Ile Lys Thr Trp Gln Ala			
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653	gat act tcc aca aca ctc tct agc atc agg tct aaa tat aaa gtc aac	1699		
657	Asp Thr Ser Thr Thr Leu Ser Ser Ile Arg Ser Lys Tyr Lys Val Asn			
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673	Pro Ile Lys Val Asp Pro Thr Met Trp Asp Thr Ile Lys Asn Asp Val			
677	535 540 545			
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701	atc tta gca ggg aaa tca gag gat gtc caa agc att gag gta caa gtc	1843		
705	Ile Leu Ala Gly Lys Ser Glu Asp Val Gln Ser Ile Glu Val Gln Val			
709	570 575 580			
717	agg gag tta ata gaa agc act act caa aaa att aaa agg gaa gag caa	1891		
721	Arg Glu Leu Ile Glu Ser Thr Thr Gln Lys Ile Lys Arg Glu Glu Gln			
725	585 590 595			
733	agt ttg aag gaa aaa atg atc att tct cca ggc agg tat ttt ctt ttg	1939		
737	Ser Leu Lys Glu Lys Met Ile Ile Ser Pro Gly Arg Tyr Phe Leu Leu			
741	600 605 610			
749	tgt cac agc agt cta ctg gac cat tta ctc acg gag tgc cca gag ata	1987		
753	Cys His Ser Ser Leu Leu Asp His Leu Leu Thr Glu Cys Pro Glu Ile			
757	615 620 625			

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781	agt gca gat gtg tat aaa gca aag tgt gaa atc cag gaa aag gtg tac	2083
785	Ser Ala Asp Val Tyr Lys Ala Lys Cys Glu Ile Gln Glu Lys Val Tyr	
789	650 655 660	
797	acc atg gct cag aaa aac att cag gtt tct cct gag att ttt cag ttt	2131
801	Thr Met Ala Gln Lys Asn Ile Gln Val Ser Pro Glu Ile Phe Gln Phe	
805	665 670 675	
813	ttg caa cag gta aac tgg aaa gaa ttc tct aag tgt ctt ttc ata gca	2179
817	Leu Gln Gln Val Asn Trp Lys Glu Phe Ser Lys Cys Leu Phe Ile Ala	
821	680 685 690	
829	cag aag att ctt gca ctt tat gag cta gag ggt aca act gtt ctc tta	2227
833	Gln Lys Ile Leu Ala Leu Tyr Glu Leu Glu Gly Thr Thr Val Leu Leu	
837	695 700 705	
845	acc agc tgt tct tct gaa gcc ctg tta gaa gca gaa aag caa atg ctc	2275
849	Thr Ser Cys Ser Ser Glu Ala Leu Leu Glu Ala Glu Lys Gln Met Leu	
853	710 715 720 725	
861	agt gcc tta aat tat aag cgc att gaa gtt gag aac aaa gaa gtt ctt	2323
865	Ser Ala Leu Asn Tyr Lys Arg Ile Glu Val Glu Asn Lys Glu Val Leu	
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877	cat ggc aag aaa tgg aaa ggg ctc act cac aat ttg ctt aag aaa caa	2371
881	His Gly Lys Lys Trp Lys Gly Leu Thr His Asn Leu Leu Lys Lys Gln	
885	745 750 755	
893	aat tcc tcc cca aac act gta atc atc aat gag tta act tca gaa acc	2419
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901	760 765 770	
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933	790 795 800 805	
941	ctg gtt gaa gta aag cct tcc tta gtt att gac tat tta aag aca gaa	2563
945	Leu Val Glu Val Lys Pro Ser Leu Val Ile Asp Tyr Leu Lys Thr Glu	
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957	aag aag cta ttc tgg cca aag ata aag aag gta aat gtg cag gta agt	2611
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973	ttc aat cct gag aac aaa caa aaa ggc att tta cta act ggc tca aag	2659
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993	Thr Glu Val Leu Lys Ala Val Asp Ile Val Lys Gln Val Trp Asp Ser	
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1085	gtg	gtg	gtg	aat	gca	tct	aat	gag	gac	ctt	aag	cat	tat	ggt	ggc	ctg	2995
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1185	Tyr	Lys	Tyr	Arg	Ser	Ile	Ala	Ile	Pro	Ala	Ile	Ser	Ser	Gly	Val		
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1277	aca	tca	tgg	gaa	aaa	gga	agc	ctg	gtg	tcc	ccg	gga	ggc	ctg	cag		3541
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VERIFICATION SUMMARY

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L:45 M:270 C: Current Application Number differs, Replaced Current Application No

L:45 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:113 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:105